**Molecular Dynamic Project explained**

With the AMBER software, molecular dynamics (MD) simulations were conducted on the GFP protein using various parameters. The resulting trajectories were visualized using Chimera software. MD simulations are essential for assessing the stability and favorability of atoms within a protein or molecular system over time.

The project aims to demonstrate how modifications to simulation parameters and raw input data impact the outcome of MD simulations.

Key points:

* Data was sourced from the internet and underwent a preliminary energy minimization step to prepare it for simulation.
* This project showcases my proficiency in working within a Linux environment, utilizing high-performance computing, writing bash scripts, and employing data visualization techniques.
* The 'MD Various Conditions' folder contains bash scripts for simulations and resultant data files generated with different MD input parameters.
* For efficiency, the largest trajectory files (.nc) and computer readable coordinates files (.rst7) produced by the Amber software were removed to reduce the zip file size.